



UniGene

ORGANISED VIEW OF THE TRANSCRIPTOME

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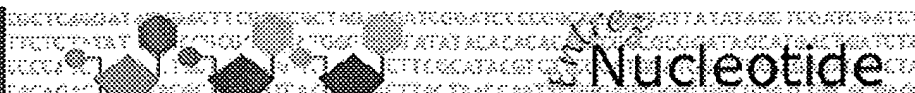
NCBI

**EST, clone IMAGE:300515, 5'end**[UniGene](#)[Homepage](#)[Query Tips](#)[FAQs](#)[DDD](#)[Download UniGene](#)[Related](#)[Resources](#)[HomoloGene](#)[dbEST](#)[Trace Archive](#)[BLAST](#)[CGAP](#)[MGC cDNA clones](#)**SEQUENCE INFORMATION**GenBank entry: [W07459.1](#)

Sequence length: 241 bases

Clone: IMAGE:300515

Library: [Soares\\_fetal\\_lung\\_NbHL19W](#)  
[dbEST 415](#)**FEATURES**[switch to text mode](#)[NLN|NIH|UniGene](#)[Privacy](#)  
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Range: from  to 
☐ Reverse complemented strand
 Features: ☐ SNP

☐ CDD
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 ☐ HPRD
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☐ 1: [W07459](#). Reports za97f06.rl Soares...[gi:1281460] [Links](#)

LOCUS W07459 241 bp mRNA linear EST 25-APR-1996  
 DEFINITION za97f06.rl Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone  
 IMAGE:300515 5', mRNA sequence.  
 ACCESSION W07459  
 VERSION W07459.1 GI:1281460  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 241)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
 ,R., Williamson,A., Wohldmann,P. and Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 164.  
 FEATURES Location/Qualifiers  
 source 1..241  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1245439"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:300515"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGAATTTTTTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

## ORIGIN

```
1  tcagtttaag aatgcttaat tcctagatga actaagagtg tttattacat gttgagattt
61  atggtatgct ttttcttcct caagataatg cattttttgt attatctgtt aatgtgatag
121 ggtaaccnat tggggaattt ncaatcattg aacaaccctt gatttttttg gataaaactct
181 attnggtcat tatgcatcat tctataaacc ctgctgaant tttcatttgc caacatctta
241 t
```

//

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Feb 9 2005 14:31:10



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MGC cDNA clones

### SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest function of a gene.

<i>D. melanogaster</i>	pir:S15008 - S15008 gene disco protein - fruit fly	27.74 % / 349 aa (see ProtEST)
<i>H. sapiens</i>	pir:A46415 - A46415 basonuclein - human	99.80 % / 993 aa (see ProtEST)
<i>M. musculus</i>	sp:O35914 - BASO_MOUSE Zinc finger protein basonuclein	86.84 % / 964 aa (see ProtEST)

### GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

cDNA sources: brain, colon, liver, lung, prostate, uterus, embryo, juvenile, adult

Expression Profile: View expression levels using UniGene's EST ProfileViewer

GEO profiles: Gene expression profiles in the NCBI Gene Expression Omnibus database

### MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Genome View: 10

UniSTS entry: D11S4421

### SEQUENCES

Sequences representing this gene; mRNAs, ESTs, and gene predictions supported by transcribed sequences.

#### EST Sequences (12)

CB133377.1	Clone L9SNU354-11-G07	liver	5' read
AI357412.1	Clone IMAGE:1963465	colon	3' read A
AI590539.1	Clone IMAGE:2259360	brain	3' read A
R45447.1	Clone IMAGE:35226	brain	3' read PA
AI870708.1	Clone IMAGE:2428099	uterus	3' read A
H09991.1	Clone IMAGE:46810	brain	3' read PA

BF222169.1	Clone IMAGE:3648501	prostate	3' read A
BF754676.1	Clone (no-name)	colon	
BF754824.1	Clone (no-name)	colon	
BF758462.1	Clone (no-name)	colon	
BF802655.1	Clone (no-name)	colon	
W07459.1	Clone IMAGE:300515	lung	5' read

**Key to Symbols****P** Has similarity to known Proteins (after translation)**A** Contains a poly-Adenylation signal**S** Sequence is a Suboptimal member of this cluster**M** Clone is putatively CDS-complete by MGC criteria**DOWNLOAD SEQUENCES**

There will be a pause of up to one minute before your computer receives any data. The default filename will be "download" If your operating system responds to filename suffixes, remember to choose a suffix compatible with plain text or fasta formats.

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Links

**D11S4421***Homo sapiens* chromosome 11, locus MGC16207*Pan troglodytes* chromosome 11Found by e-PCR in sequences from *Homo sapiens* and *Pan troglodytes*.

## Related sites

e-PCR

Map Viewer

Gene

UniGene

dbSNP

GeneMap'99

RHdb

GDB

MGD

ZFIN

**Primer Information**

Forward primer: TTAATCCTCAGTACATTTTCAACCC  
 Reverse primer: TGATGCGCTACCTTGCTTC  
 PCR product size: 157-158 (bp), *Homo sapiens*  
 GenBank Accession: G06217 Z38424

***Homo sapiens***

Name: D11S4421  
 Also known as: HSC0BA112 WI-6395

## Genomic biology

*Bos taurus**Canis familiaris**Danio rerio**Homo sapiens**Mus musculus**Rattus norvegicus**Sus scrofa***Cross References**

Gene GenelD: 84853  
 Symbol: MGC16207  
 Description: hypothetical protein MGC16207  
 Position: 11q23.3  
 UniGene Hs.334846 Poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)  
 Hs.389988 Transcribed locus  
 RHdb RH52164  
 GDB GDB:678812 G00-678-812

**Mapping Information**

D11S4421 Sequence Map: Chr 11 Map Viewer  
 Position: 119036949-119037106 (bp)  
 D11S4421 Sequence Map: Chr 11|Celera Map Viewer  
 Position: 119187059-119187216 (bp)  
 WI-6395 WI-RH Map: Chr 11 Map Viewer  
 Position: 546.7 (cR3000)  
 Lod score: P0.01

WI-6395      GM99-GB4 Map:      Chr 11      Map Viewer  
Position:      391.79 (cR3000)  
Lod score:      0.80  
Reference Interval:      D11S924-D11S925 (120.8-123.5 cM)

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### Electronic PCR results



#### mRNA (5)

BC007379.2	1211 .. 1368
BC021976.2	892 .. 1049
BC044230.2	839 .. 996
BC064140.1	836 .. 993
BC086309.1	823 .. 980

#### Genomic (5 of 6)[Show All Hits]

G06217.1	30 .. 187
AP003393.1	86597 .. 86754
CH003458.1	116187059 .. 116187216
CH003482.1	120411045 .. 120411202
CH003506.1	122254429 .. 122254586

#### Working Draft phase 1 (from GenBank HTGS division) (1)

AC036174.2	127290 .. 127447
------------	------------------

#### ESTs (5 of 72)[Show All Hits]

T10063.1	42 .. 199
Z38424.1	30 .. 187
T30207.1	35 .. 192
T85069.1	35 .. 193
T89458.1	35 .. 191

#### Whole Genome Shotgun sequences (3)

AADD01119913.1	12591 .. 12748
AADB01067920.1	5917 .. 6074
AADC01102571.1	11092 .. 11249

### *Pan troglodytes*

Name:      D11S4421

---

### Mapping Information



D11S4421	Sequence Map:	Chr 11	Map Viewer
	Position:	121054383-121054539 (bp)	

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**Electronic PCR results****Whole Genome Shotgun sequences (2)**

AADA01244170.1	3595 .. 3751
AACZ01211643.1	3611 .. 3767

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